

# Report

	pacbio_20x.contigs	pacbio_40x.contigs	pacbio_80x.contigs	illumina_contigs	illumina_pacbio_contigs
# contigs (>= 0 bp)	27	1	1	167	6
# contigs (>= 1000 bp)	27	1	1	87	1
# contigs (>= 5000 bp)	27	1	1	62	1
# contigs (>= 10000 bp)	27	1	1	57	1
# contigs (>= 25000 bp)	26	1	1	47	1
# contigs (>= 50000 bp)	22	1	1	31	1
Total length (>= 0 bp)	4595245	4652210	4653062	4567161	4642668
Total length (>= 1000 bp)	4595245	4652210	4653062	4548539	4641722
Total length (>= 5000 bp)	4595245	4652210	4653062	4493976	4641722
Total length (>= 10000 bp)	4595245	4652210	4653062	4458325	4641722
Total length (>= 25000 bp)	4579805	4652210	4653062	4312386	4641722
Total length (>= 50000 bp)	4445810	4652210	4653062	3762852	4641722
# contigs	27	1	1	97	2
Largest contig	751503	4652210	4653062	221601	4641722
Total length	4595245	4652210	4653062	4555330	4642264
Reference length	4639675	4639675	4639675	4639675	4639675
GC (%)	50.75	50.79	50.79	50.74	50.79
Reference GC (%)	50.79	50.79	50.79	50.79	50.79
N50	272515	4652210	4653062	129054	4641722
NG50	272515	4652210	4653062	129054	4641722
N75	120355	4652210	4653062	60768	4641722
NG75	120355	4652210	4653062	59669	4641722
L50	5	1	1	14	1
LG50	5	1	1	14	1
L75	13	1	1	26	1
LG75	13	1	1	27	1
# misassemblies	8	8	8	0	6
# misassembled contigs	3	1	1	0	1
Misassembled contigs length	1061852	4652210	4653062	0	4641722
# local misassemblies	2	2	2	4	5
# scaffold gap ext. mis.	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0
# unaligned mis. contigs	0	0	0	0	0
# unaligned contigs	0 + 0 part	0 + 0 part	0 + 0 part	1 + 0 part	1 + 0 part
Unaligned length	0	0	0	542	542
Genome fraction (%)	98.922	99.998	99.998	98.142	99.983
Duplication ratio	1.001	1.003	1.003	1.000	1.001
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	4.77	0.93	0.32	1.03	8.32
# indels per 100 kbp	141.51	28.47	9.51	0.33	0.86
Largest alignment	484372	3025556	3026138	221546	3023578
Total aligned length	4595231	4652208	4653060	4554465	4638936
NA50	200683	3025556	3026138	129054	3023578
NGA50	200683	3025556	3026138	129054	3023578
NA75	110650	824278	824426	60768	572346
NGA75	110650	824278	824426	59669	572346
LA50	7	1	1	14	1
LGA50	7	1	1	14	1
LA75	15	2	2	26	2
LGA75	15	2	2	27	2

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

## Misassemblies report

	pacbio_20x.contigs	pacbio_40x.contigs	pacbio_80x.contigs	illumina_contigs	illumina_pacbio_contigs
# misassemblies	8	8	8	0	6
# contig misassemblies	8	8	8	0	6
# c. relocations	6	6	6	0	6
# c. translocations	0	0	0	0	0
# c. inversions	2	2	2	0	0
# scaffold misassemblies	0	0	0	0	0
# s. relocations	0	0	0	0	0
# s. translocations	0	0	0	0	0
# s. inversions	0	0	0	0	0
# misassembled contigs	3	1	1	0	1
Misassembled contigs length	1061852	4652210	4653062	0	4641722
# local misassemblies	2	2	2	4	5
# scaffold gap ext. mis.	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0
# unaligned mis. contigs	0	0	0	0	0
# mismatches	219	43	15	47	386
# indels	6495	1321	441	15	40
# indels (<= 5 bp)	6493	1321	441	12	37
# indels (> 5 bp)	2	0	0	3	3
Indels length	6677	1350	445	77	183

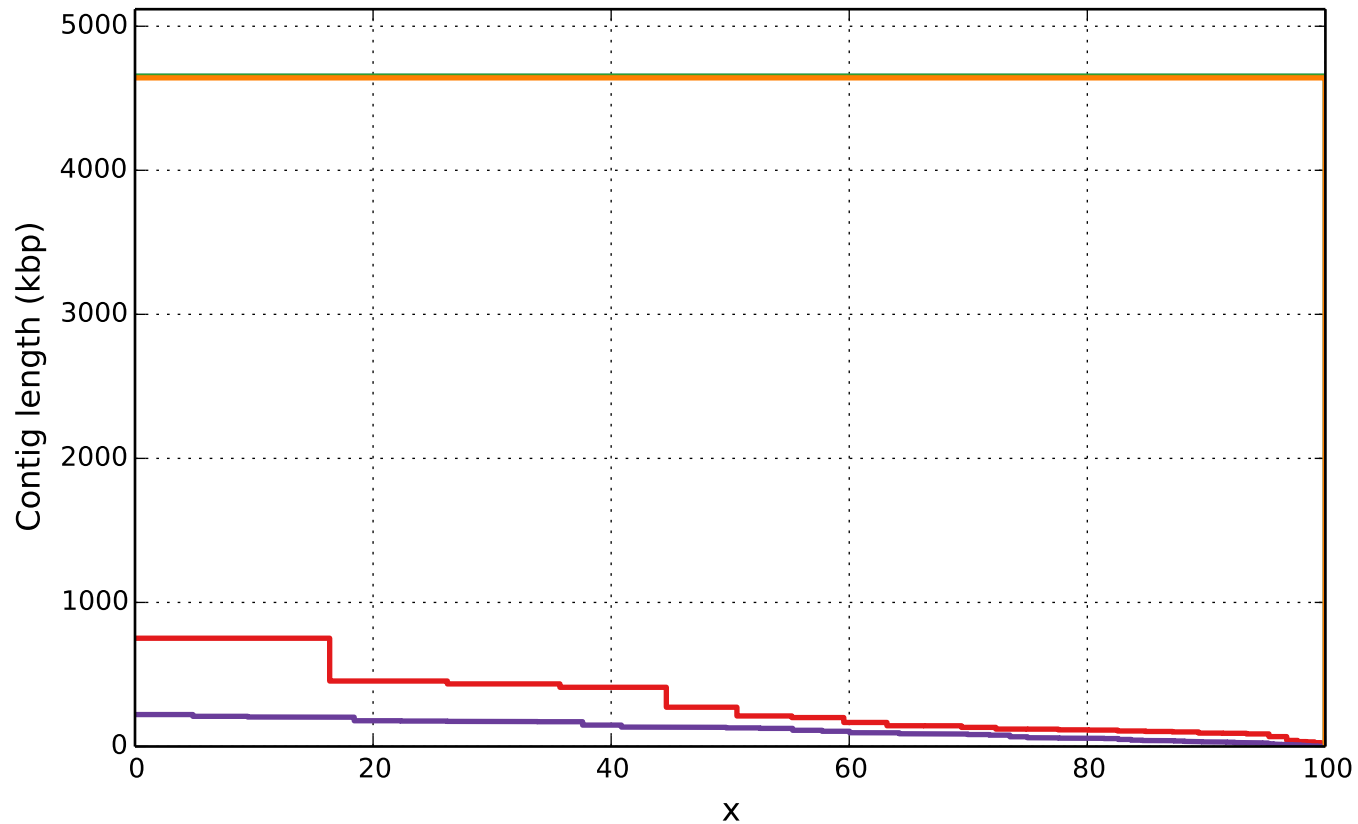
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	pacbio_20x.contigs	pacbio_40x.contigs	pacbio_80x.contigs	illumina_contigs	illumina_pacbio_contigs
# fully unaligned contigs	0	0	0	1	1
Fully unaligned length	0	0	0	542	542
# partially unaligned contigs	0	0	0	0	0
Partially unaligned length	0	0	0	0	0
# N's	0	0	0	0	0

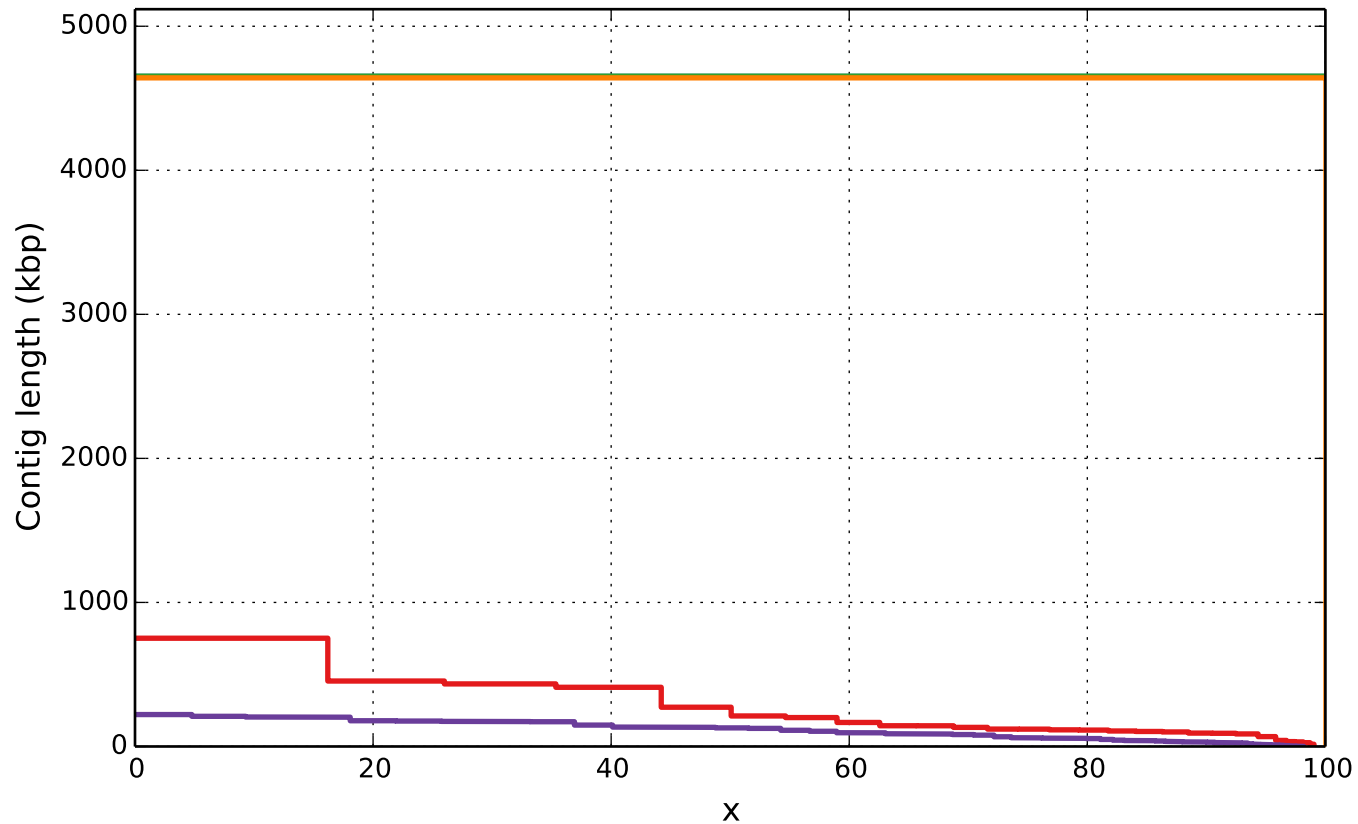
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



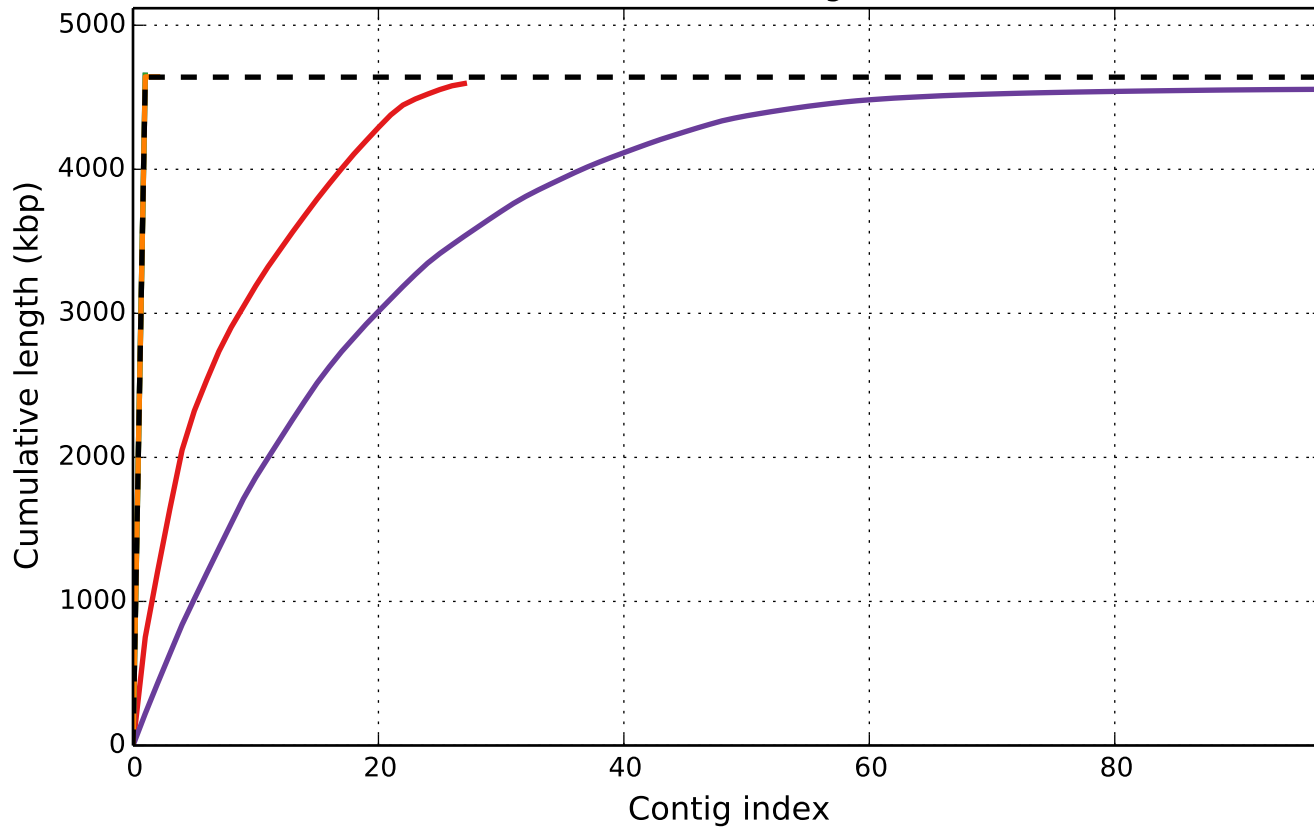
pacbio\_20x.contigs    pacbio\_80x.contigs    illumina\_pacbio\_contigs  
pacbio\_40x.contigs    illumina\_contigs

NGx



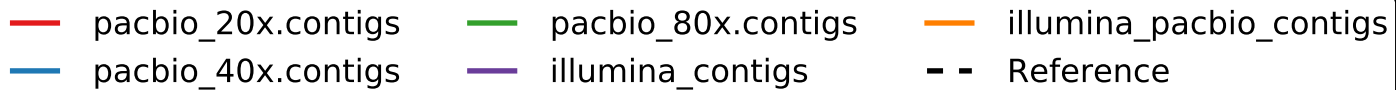
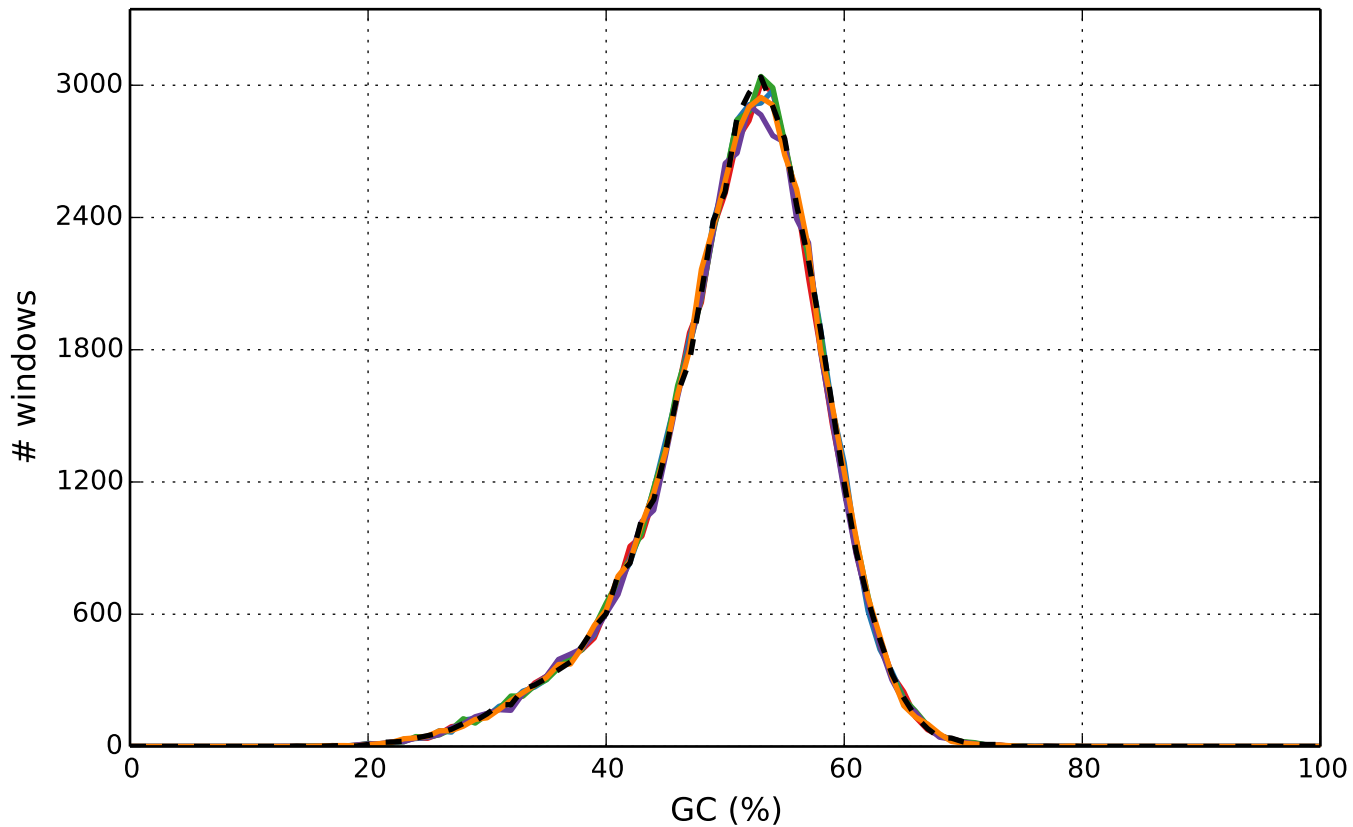
— pacbio\_20x.contigs    — pacbio\_80x.contigs    — illumina\_pacbio\_contigs  
— pacbio\_40x.contigs    — illumina\_contigs

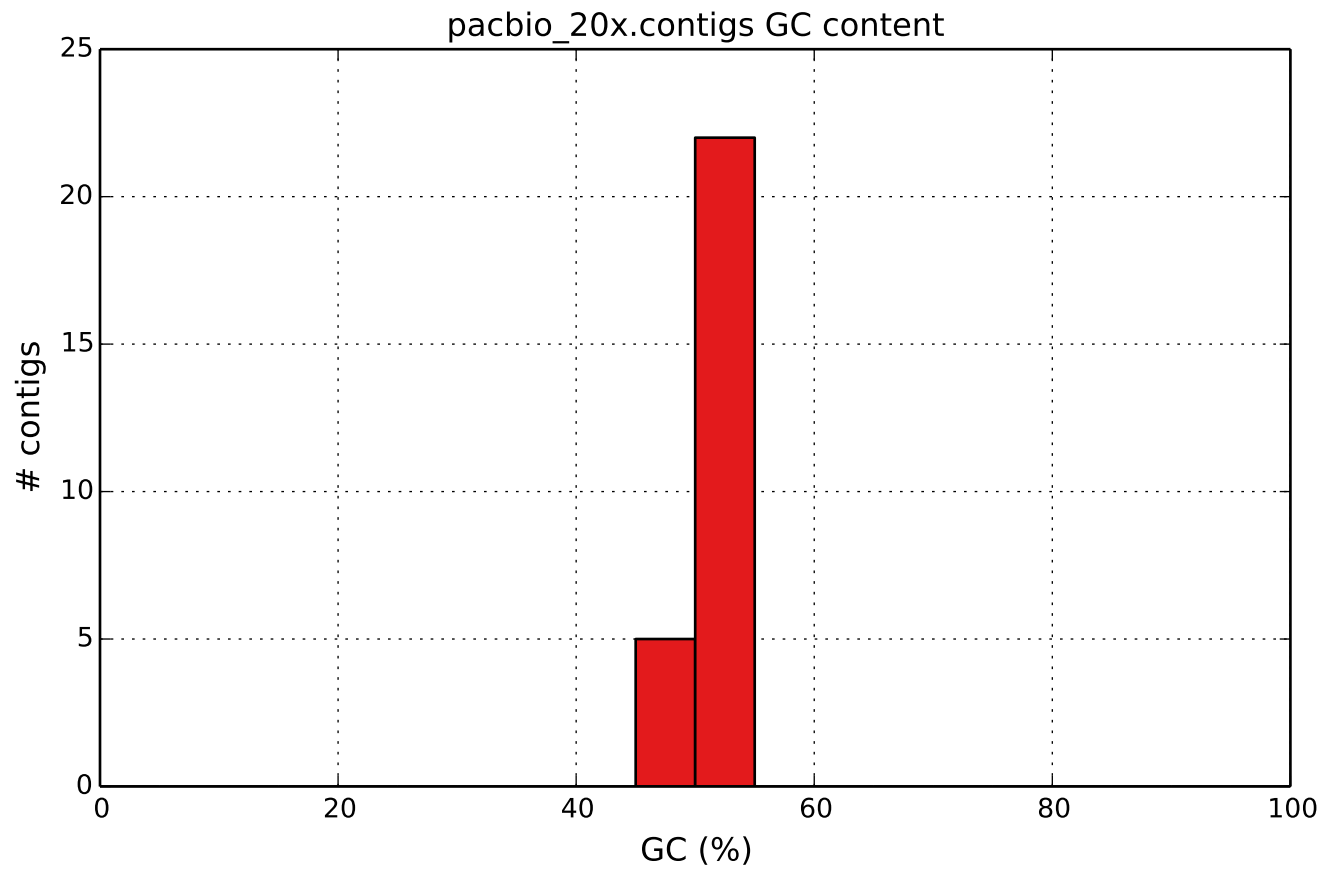
Cumulative length



pacbio_20x.contigs	pacbio_80x.contigs	illumina_pacbio_contigs
pacbio_40x.contigs	illumina_contigs	Reference

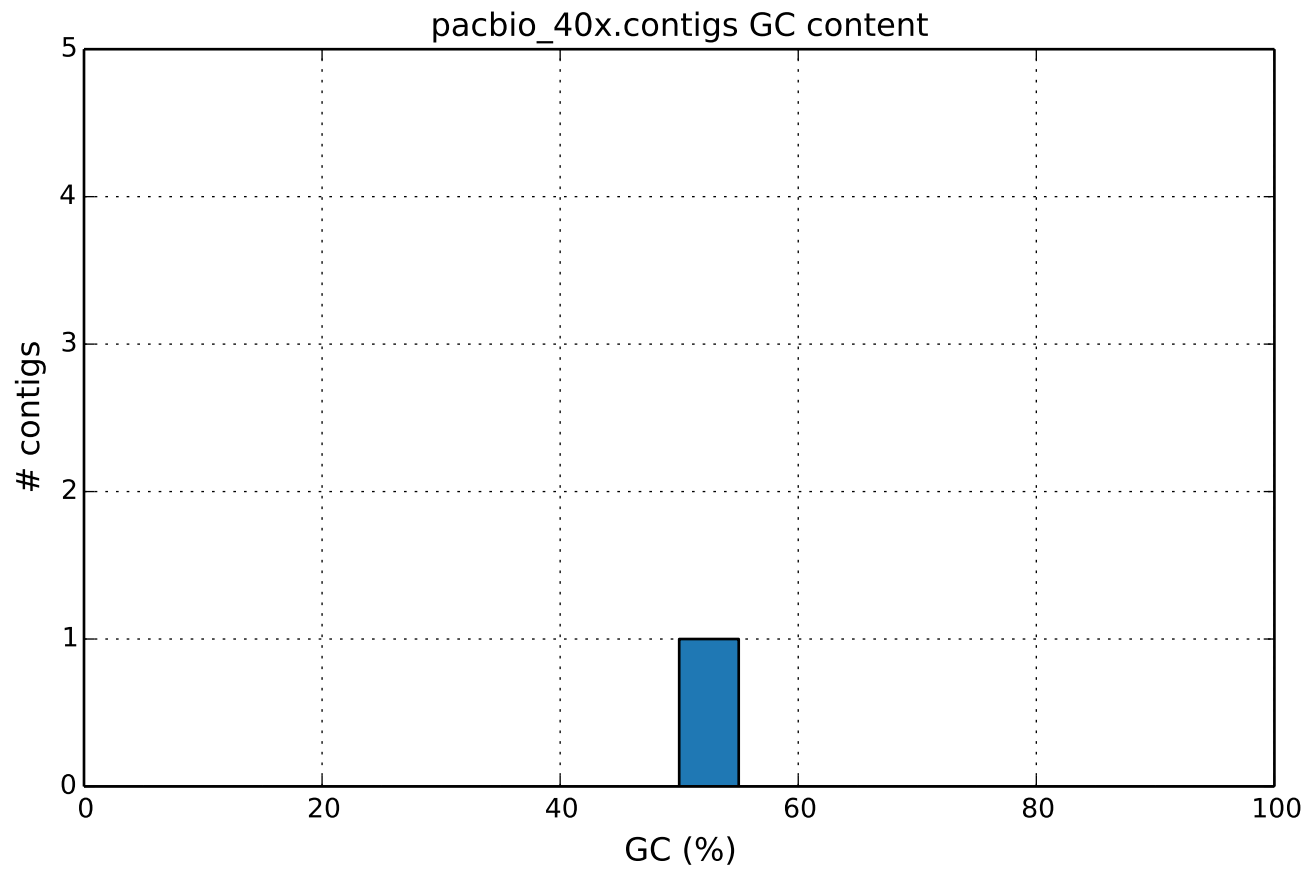
GC content



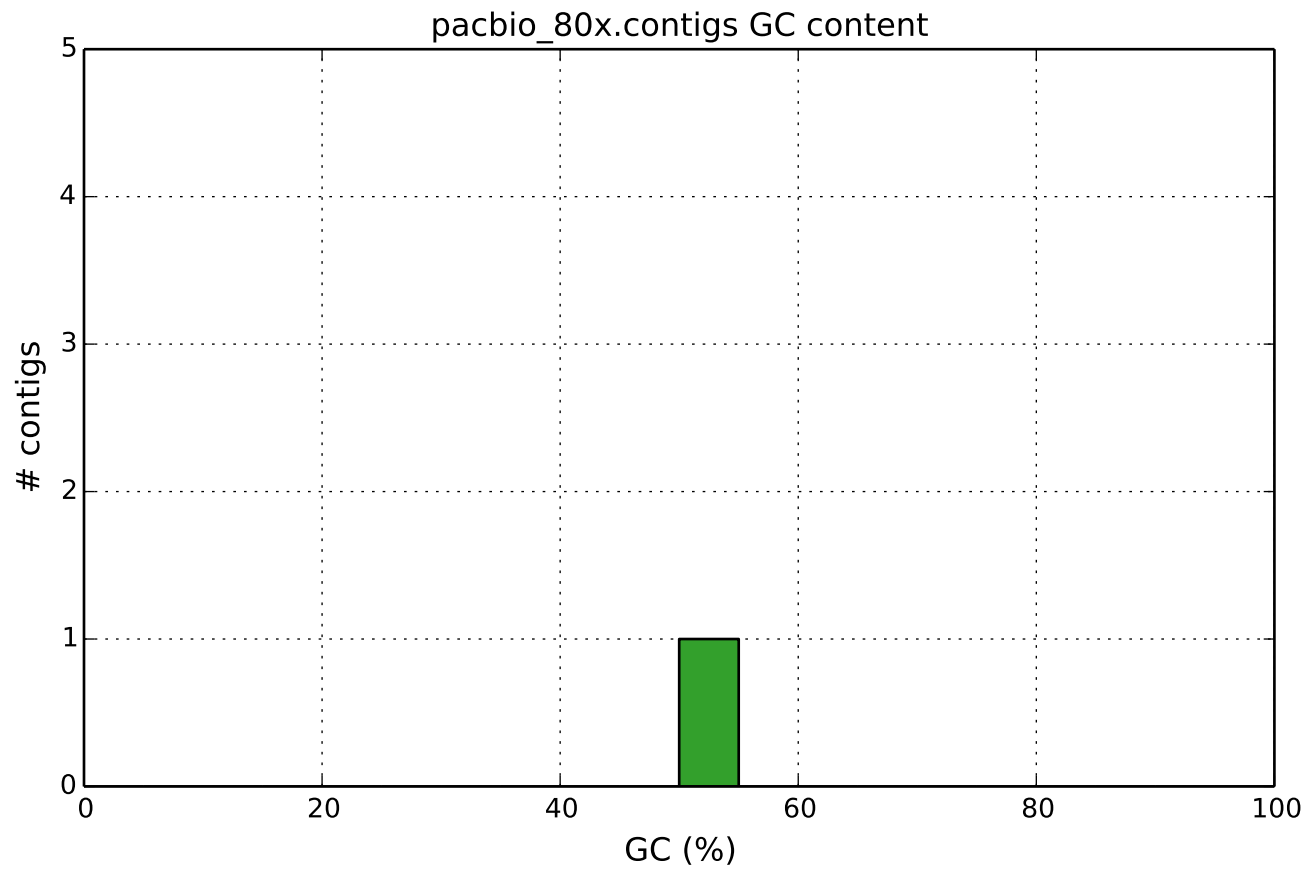


pacbio\_20x.contigs



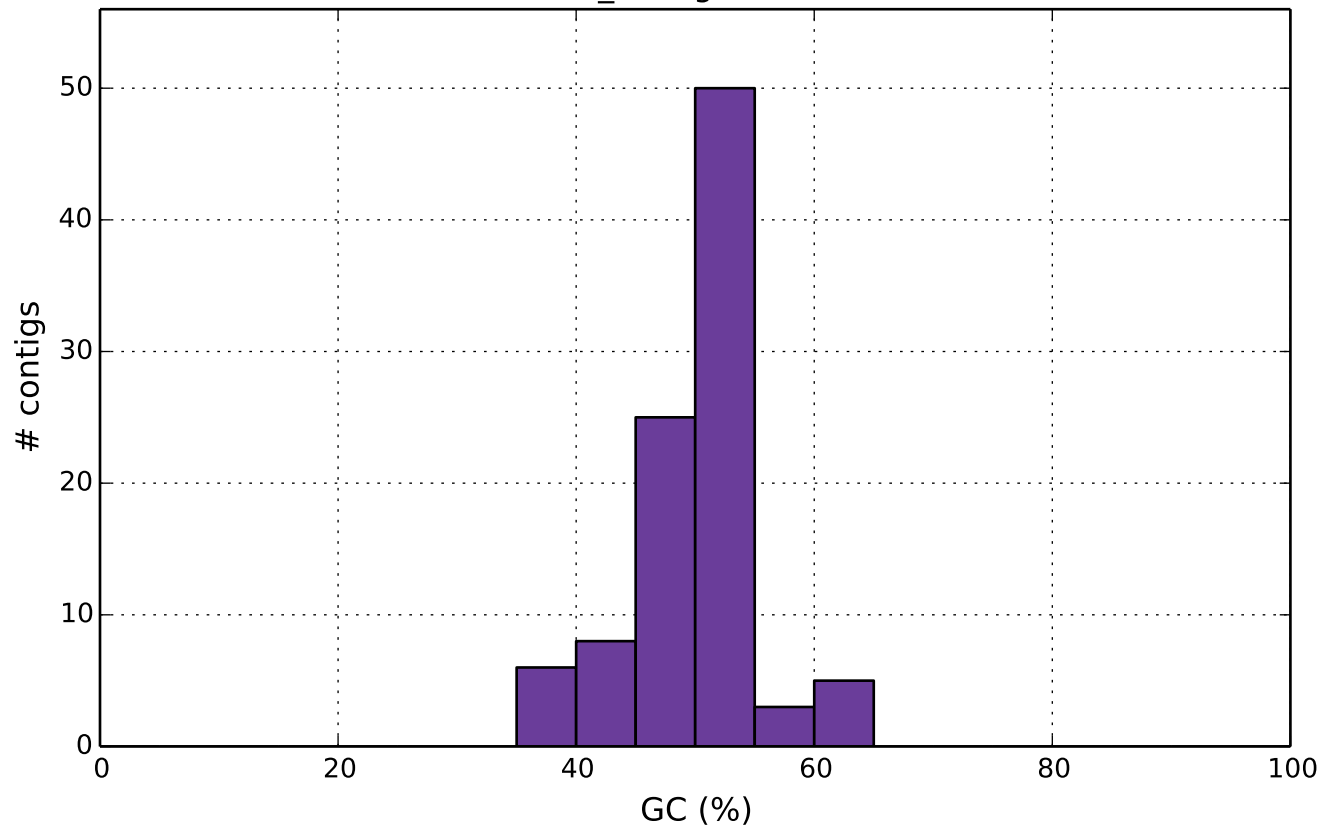


pacbio\_40x.contigs

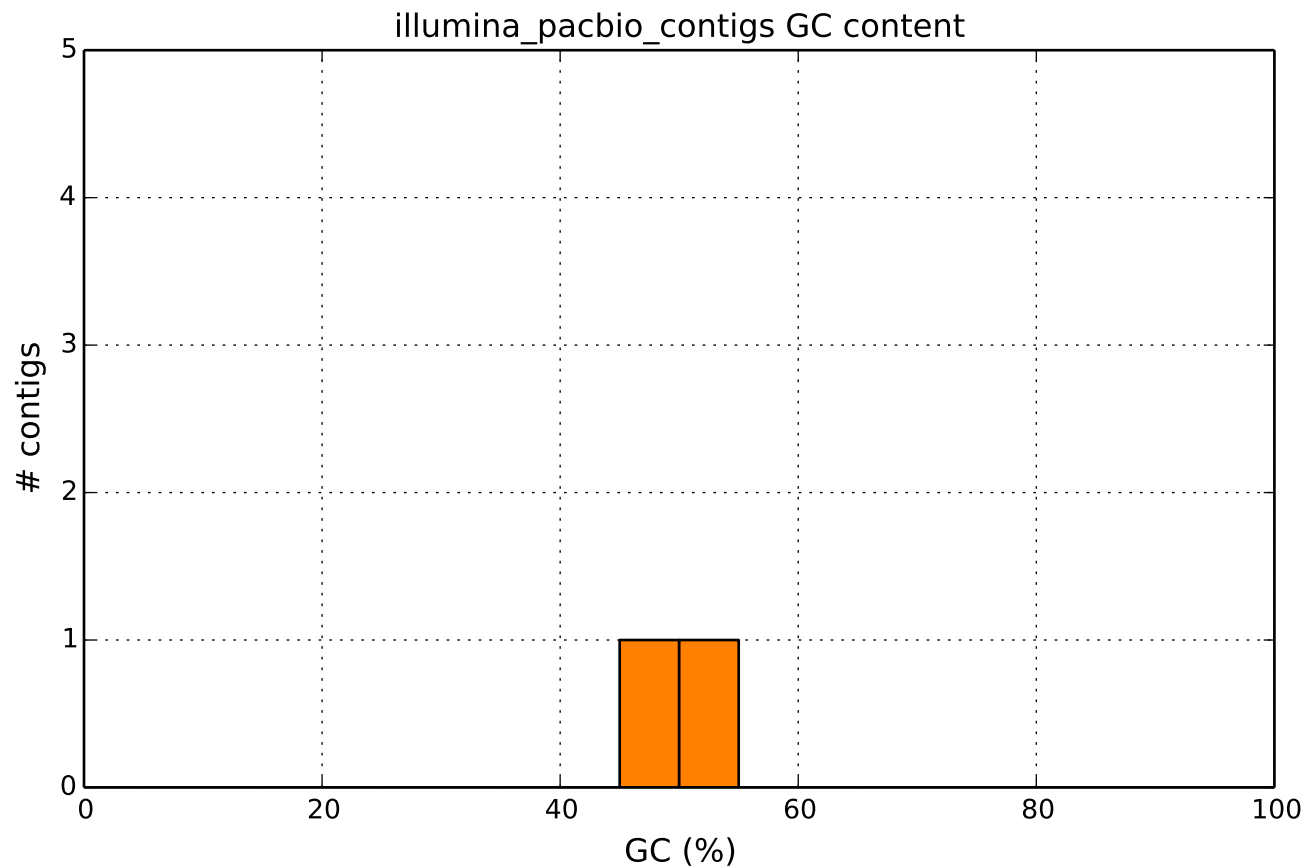



pacbio\_80x.contigs

illumina\_contigs GC content

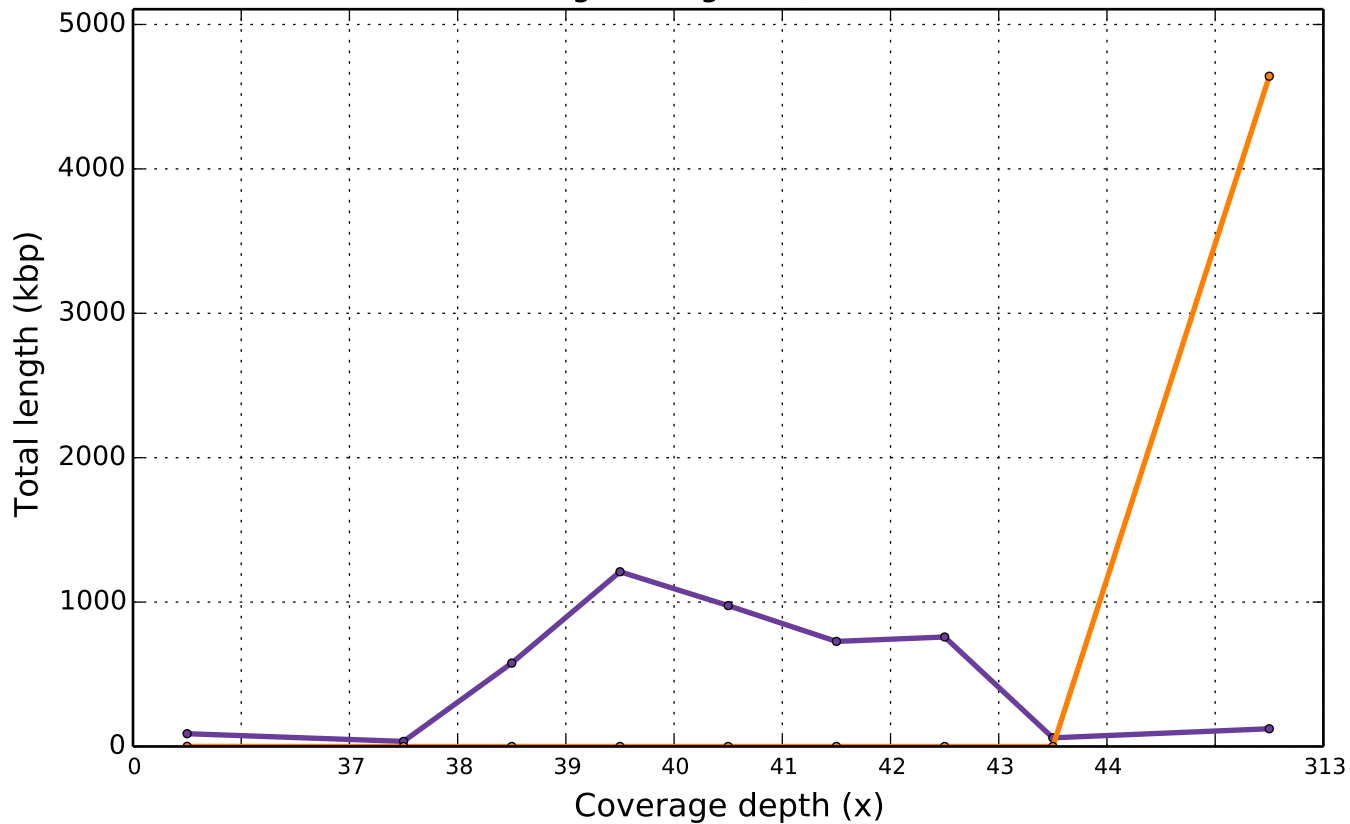


illumina\_contigs



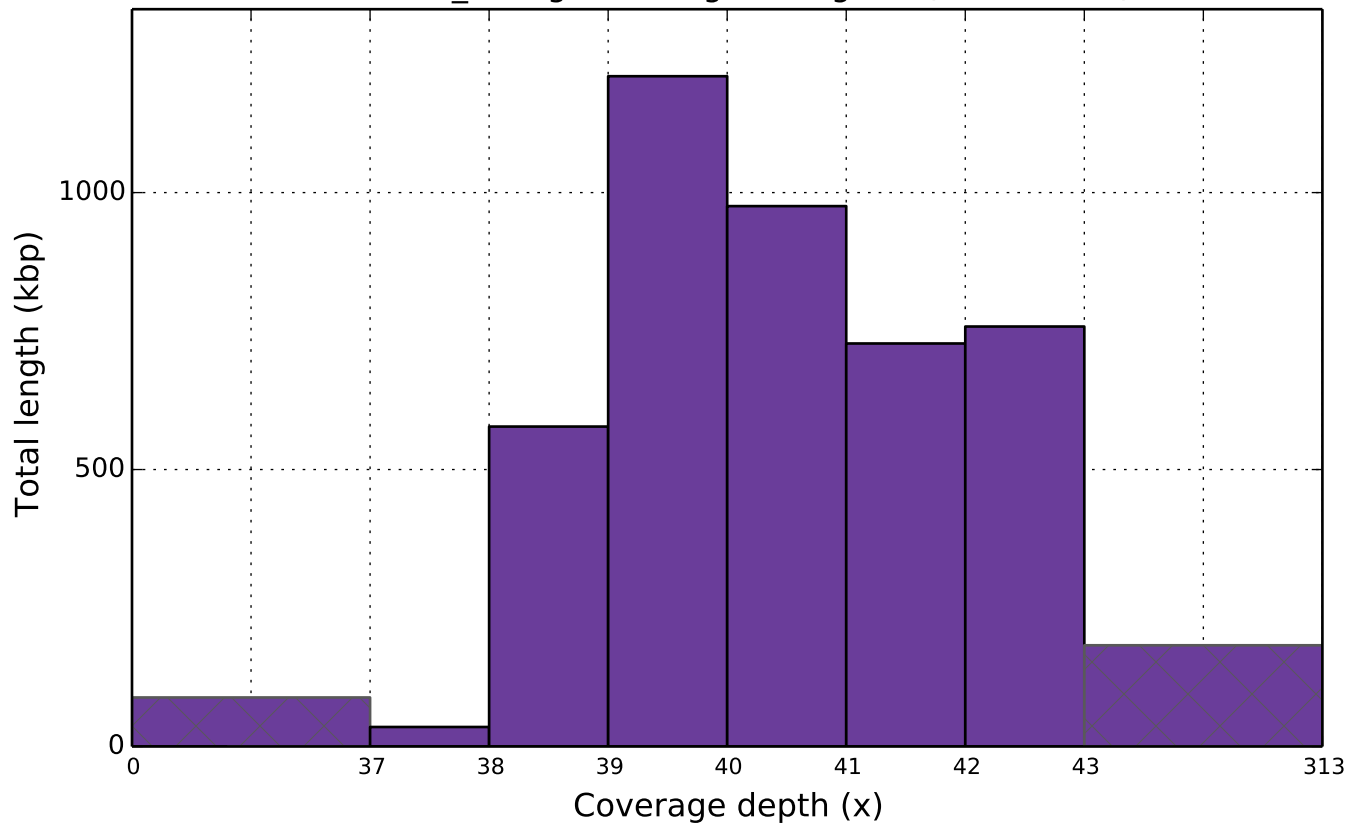
 illumina\_pacbio\_contigs

Coverage histogram (bin size: 1x)



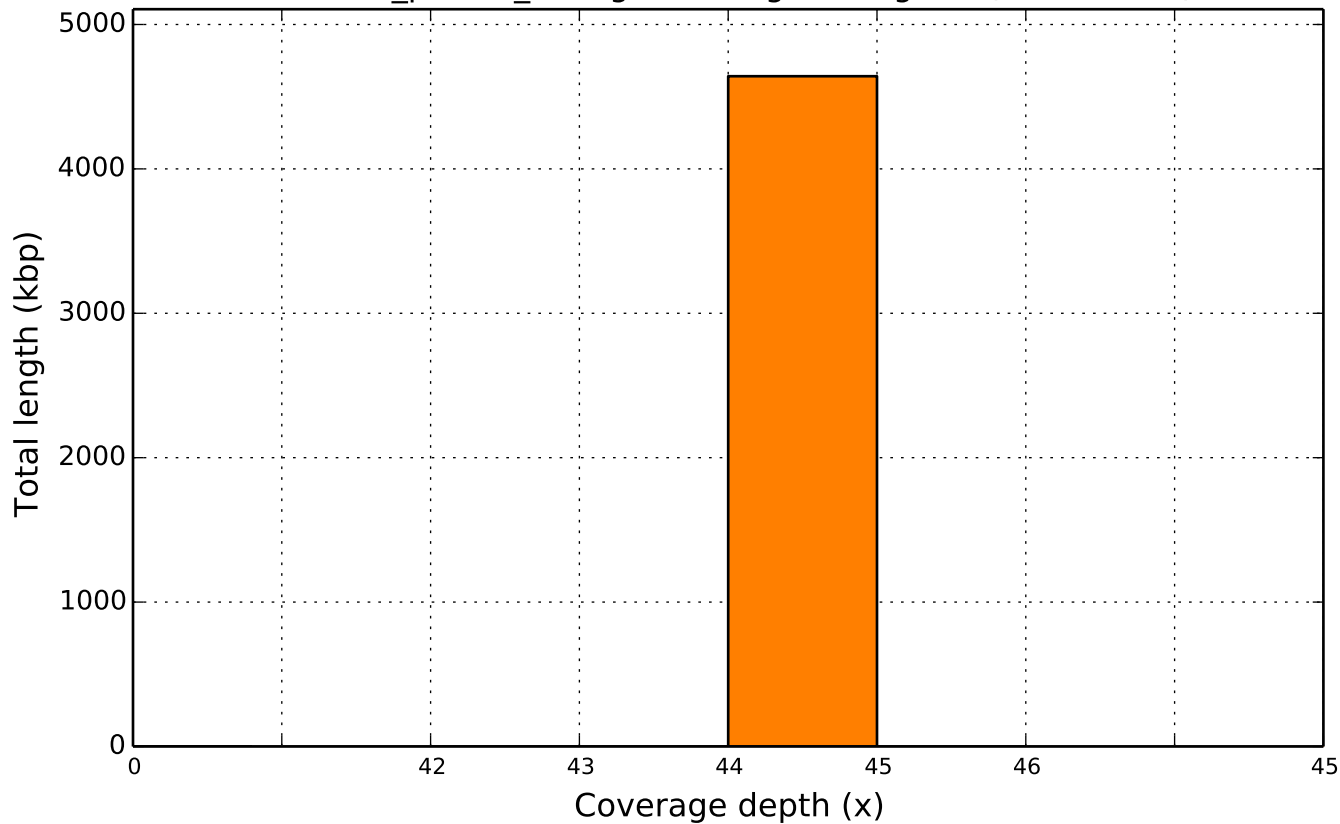
illumina\_contigs    illumina\_pacbio\_contigs

illumina\_contigs coverage histogram (bin size: 1x)



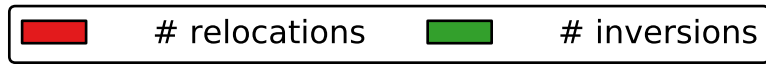
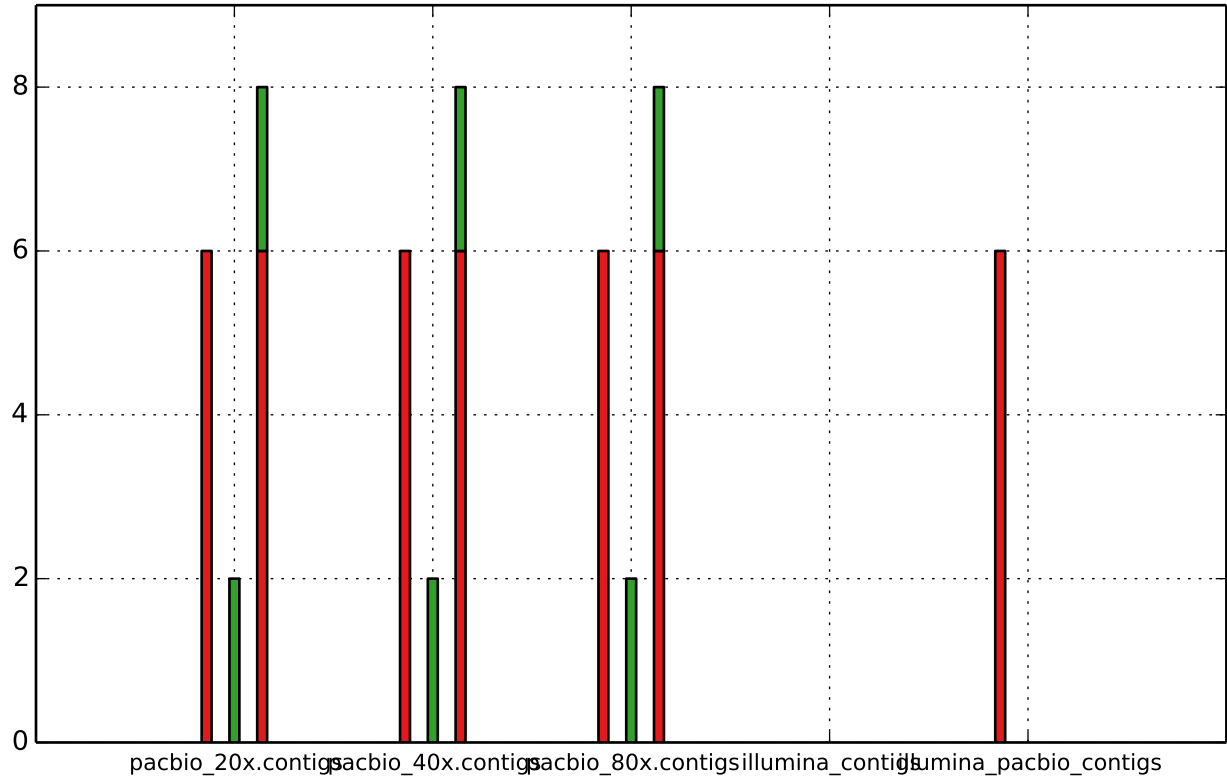
illumina\_contigs

illumina\_pacbio\_contigs coverage histogram (bin size: 1x)



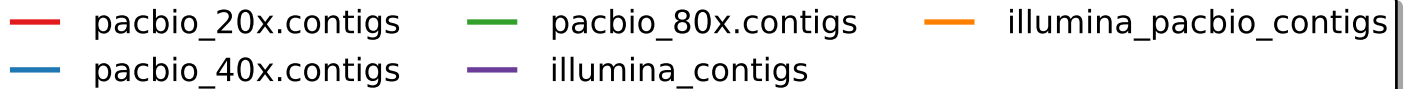
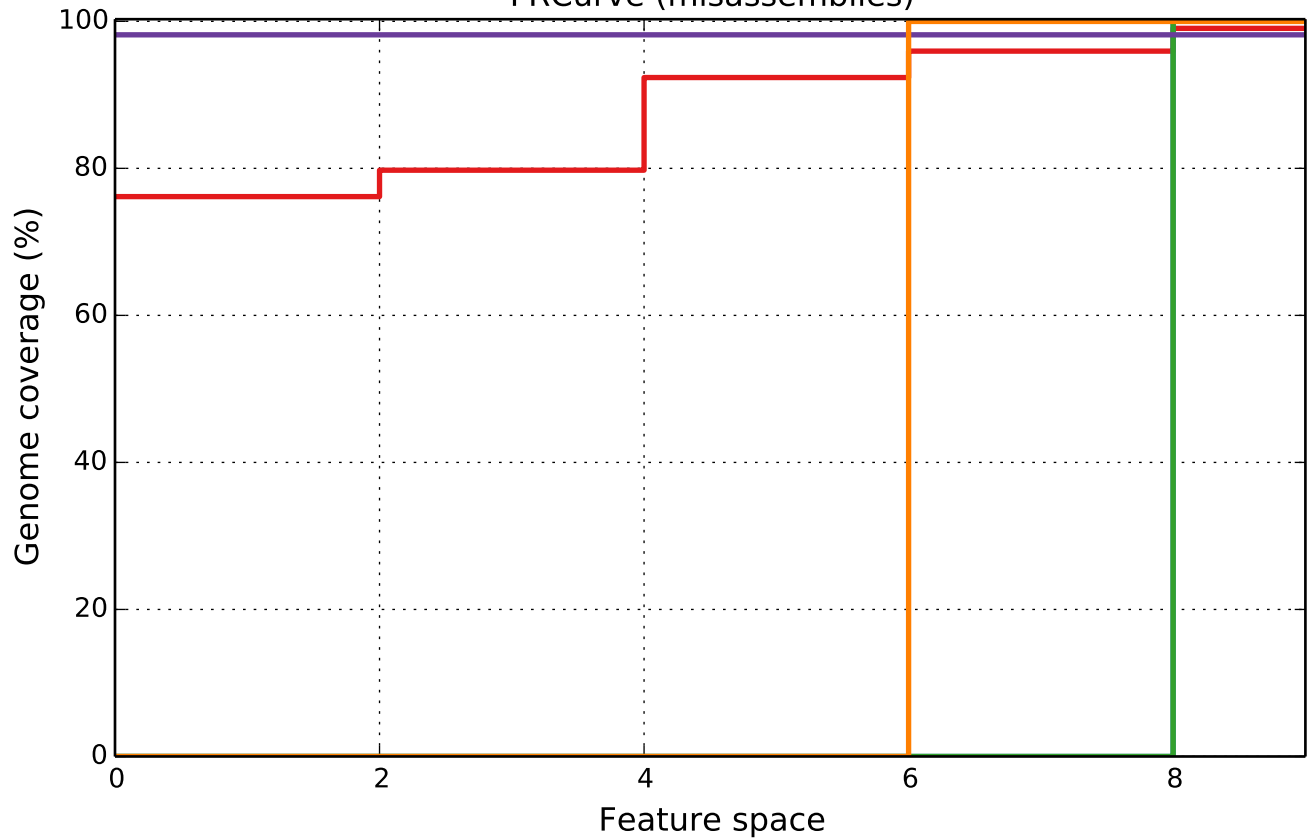
illumina\_pacbio\_contigs

# Misassemblies

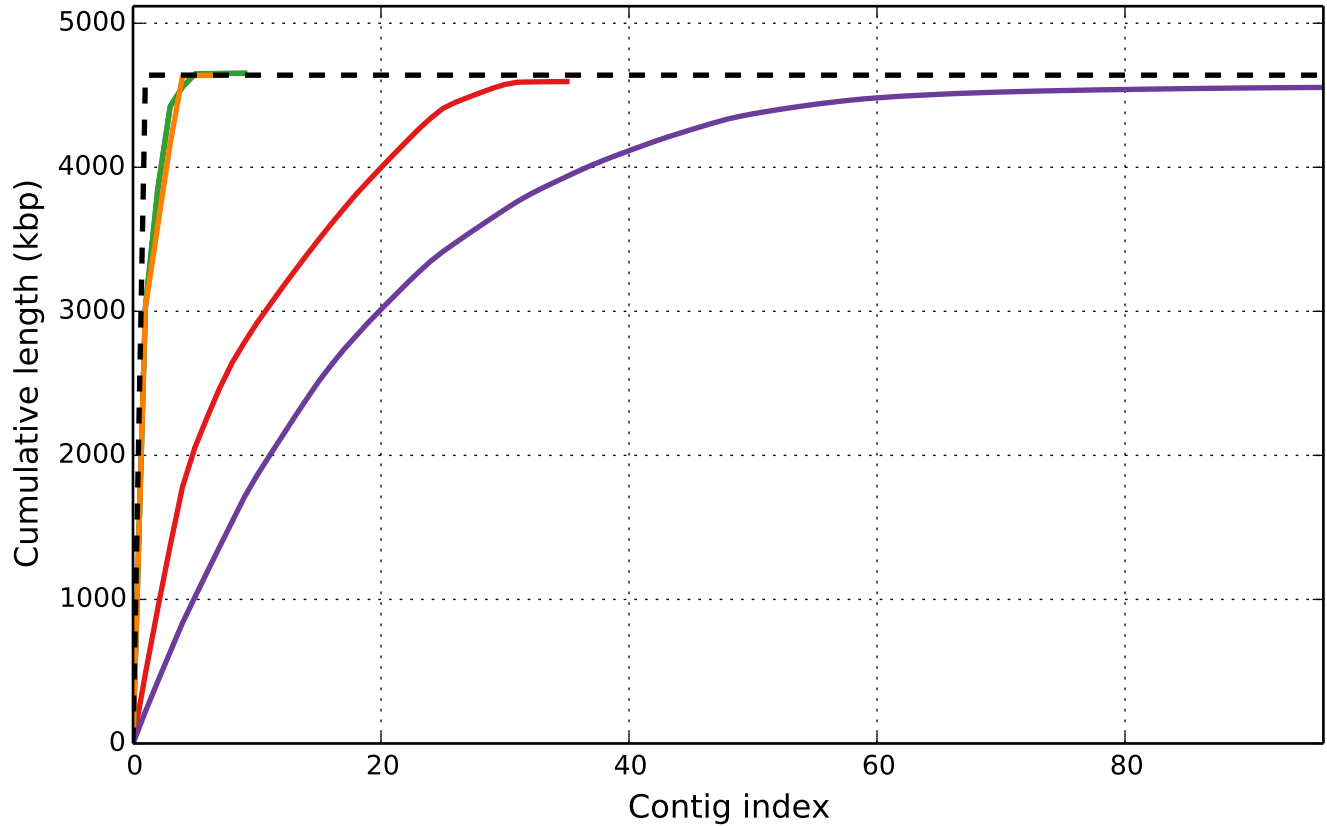




FRCurve (misassemblies)

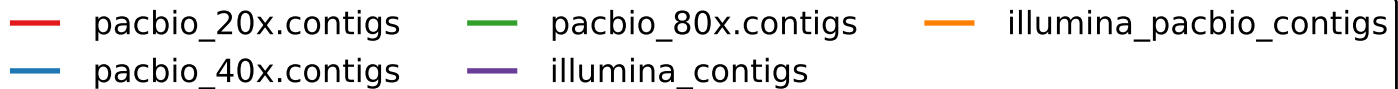
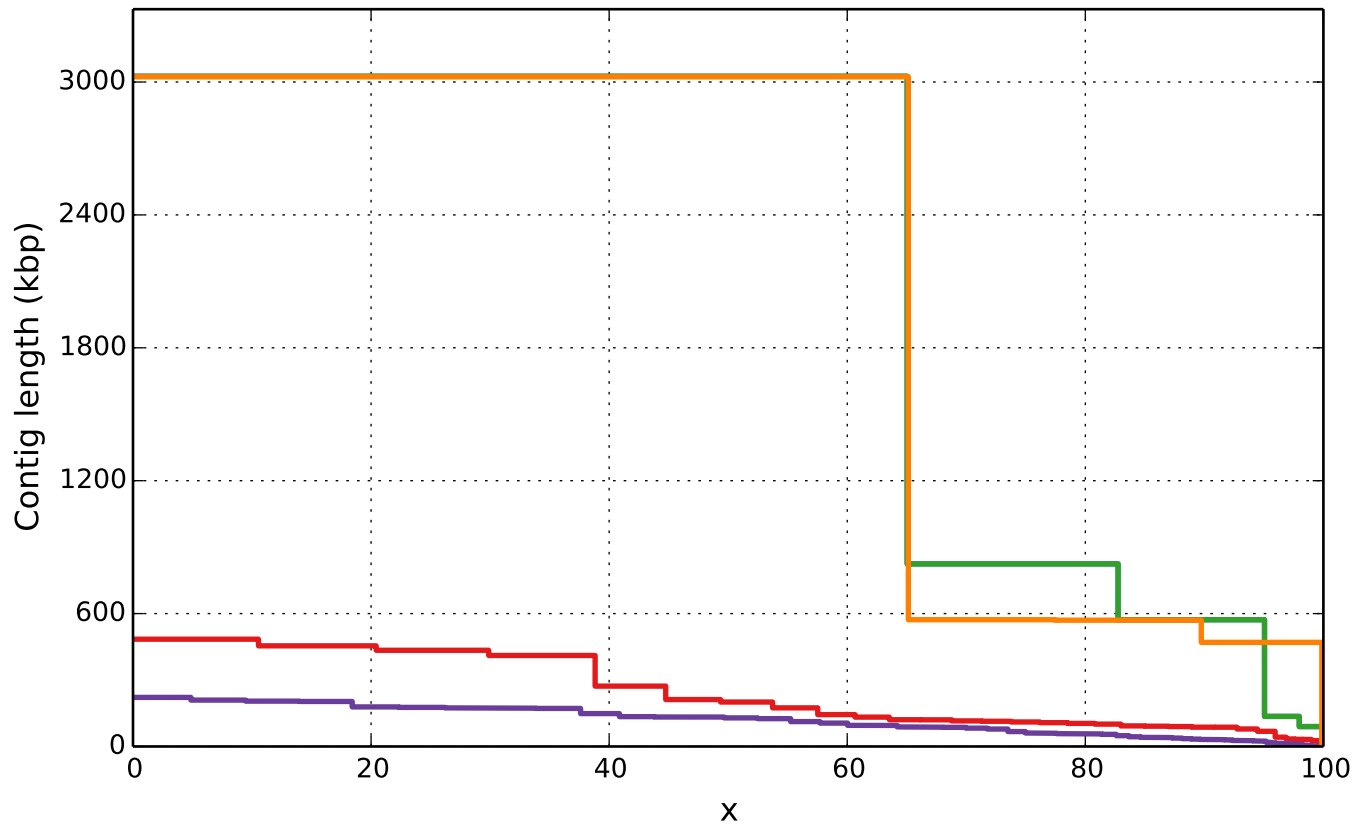


Cumulative length (aligned contigs)

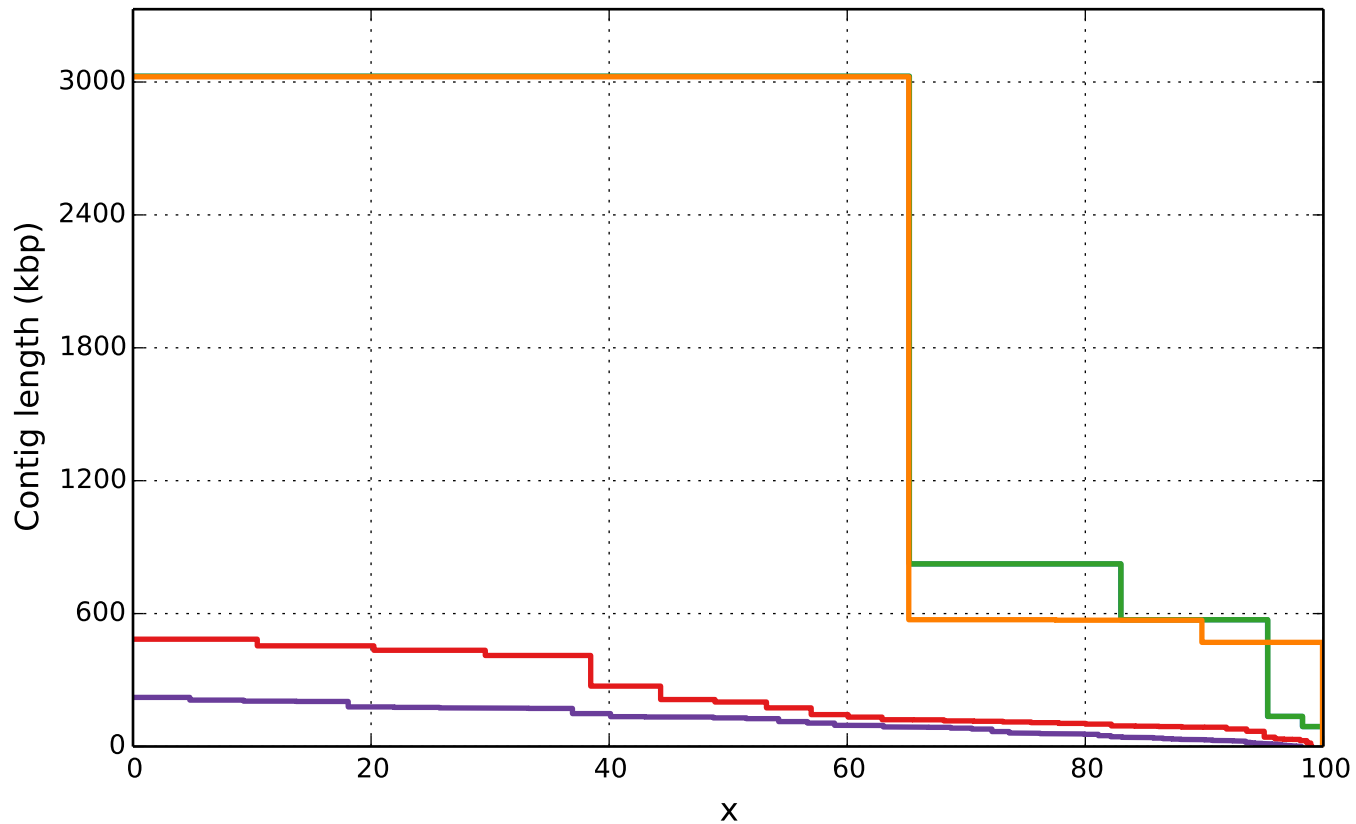


pacbio_20x.contigs	pacbio_80x.contigs	illumina_pacbio_contigs
pacbio_40x.contigs	illumina_contigs	Reference

NAx



# NGAx



- pacbio\_20x.contigs
- pacbio\_40x.contigs
- pacbio\_80x.contigs
- illumina\_contigs
- illumina\_pacbio\_contigs

